

Fig. 1a

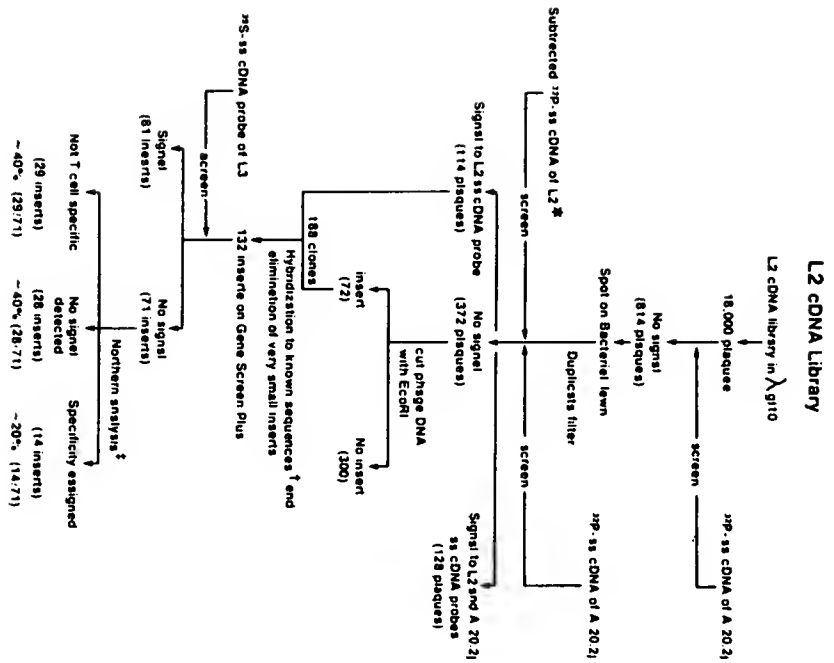


Fig. 1b

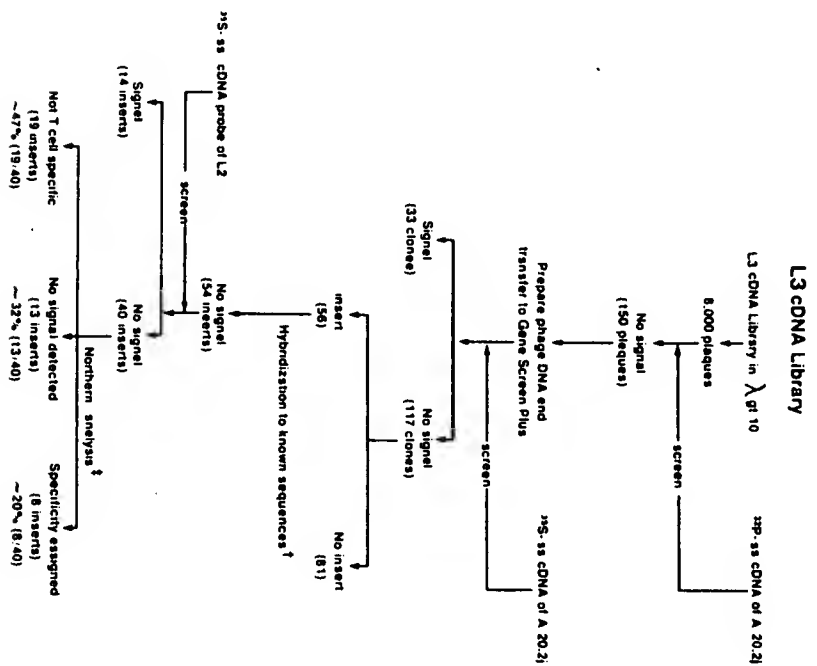


Fig. 2A

-145 ATGTC

-140 CATGAACTGC TGAGTGGATA AACAGCACGG GATATCTCTG TCTAAAGCAA TATTACTACA CCAGGAAAAG

-70 CACACATTGC ACAACAGGAA AGGAGCCTGT CACAGAAAAC CACAGTGTCC TGTGCATGTG ACATTTCGGC

1 ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG GGC TGT CAG AAG 60
1 Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val Gly Cys Glu Lys 20

61 GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TGT CAG CCT GGT ACT TTC TGC AGA AAA TAC 120
21 Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys Tyr 40

121 AAT CCA GTC TGC AAG AGC TGC CCT CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC 180
41 Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn 60

181 TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT ACC 240
61 Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr 80

241 CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA 300
81 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg 100

301 TGT GAA AAG CAC TGC AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC 360
101 Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser 120

361 TTG GGA ACA TTT AAT CAC CAG AAC GGT ACT GGC GTC TGT CCA CCC TGG ACG AAC TGC TCT 420
121 Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser 140

421 CTA GAC GGA ACG TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC 480
141 Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro 160

481 CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA 540
161 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly 180

541 GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG CTG ACA TCG GCT TTG CTG CTG GCC 600
181 Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser Ala Leu Leu Leu Ala 200

601 CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC 660
201 Leu Ile Phe Ile Thr Leu Leu Phe Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His 220

661 ATA TTC AAG CAA CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC 720
221 Ile Phe Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser 240

721 TGC CCA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGA GGC TAT GAG CTG TGA TGTACTATC 780
241 Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu ---

Fig. 2B

781 CTAGGAGATG TGTGGGCCGA AACCGAGAAG CACTAGGACC CCACCATCCT GTGGAACAGC ACAAGCAACC 850
851 CCACCACCCT GTTCTTACAC ATCATCCTAG ATGATGTGTG GCGCGGCACC TCATCCAAGT CTCTTCTAAC 920
921 GCTAACATAT TTGTCITTAC CTTTTTAA TCTTTTTTA AATTAAATT TTATGTGTGT GAGTGTITG 990
991 CCTGCCTGTA TGCACACGTG TGTGTGTGTG TGTGTGTGAC ACTCCTGATG CCTGAGGAGG TCAGAAGAGA 1060
1061 AAGGGTTGGT TCCATAAGAA CTGGAGTTAT GGATGGCTGT GAGCCGnnn GATAGGTCGG GACGGAGACC 1130
1131 TGTCTTCTTA TTTTAACGTG ACTGTAT AAT AAAAAAAAA TGATATTTCC GGAATTGTAG AGATTGTCCT 1200
1201 GACACCCCTC TAGTTAATGA TCTAAGAGGA ATTGTTGATA CGTAGTATAC TGTATATGTG TATGTATATG 1270
1271 TATATGTATA TATAAGACTC TTTTACTGTC AAAGTCAACC TAGAGTGTCT GGTACCAGG TCAATTTTAT 1340
1341 TGGACATTTT ACGTCACACA CACACACACA CACACACACA CACGTTTATA CTACGTACTGT TATCGGTAT 1410
1411 TCTACGTCAT ATAATGGGAT AGGATAAAAG GAAACCAAAG AGTGAGTGAT ATTATTGTGA GGTGACAGA 1480
1481 CTACCCCTTC TGGGTACGTA GGGACAGACC TCCTTCGGAC TGTCTAAAC TCCCCTTAGA AGTCTCGTCA 1550
1551 AGTTCCTCGA CGAAGAGGAC AGAGGAGACA CAGTCCGAAA AGTTATTTT CCGGCAAAATC CTTTCCCTGT 1620
1621 TTCTGTACAC TCCACCCCTT GTGGACACTT GAGTGTATC CTTGCGCCGG AAGGTCAGGT GGTACCCGTC 1690
1691 TGTAGGGGGG GGGAGACAGA GCGCGGGGG AGCTACGAGA ATCGACTCAC AGGGCGCCCC GGGCTTCGCA 1760
1761 AATGAAACTT TTTTAATCTC ACAAGTTTCG TCCGGGCTCG GCGGACCTAT GCGTTCGATC CTTATTACCT 1830
1831 TATCCTGGCG CCAAGATAAA ACAACAAAA GCCTTGACTC CGGTACTAAT TCTCCTGCC GCGCCCCGTA 1900
1901 AGCATAACGC GCGATCTCC ACITTAAGAA CCTGGCGCGG TTCTGCCTGG TCTCGCTTTC GTAAACGGTT 1970
1971 CTTACAAAAG TAATTAGTTC TTGCTTTCAG CCTCCAAGCT TCTGCTAGTC TATGGCAGCA TCAAGGCTGG 2040
2041 TATTTCGTAC GGCTGACCGC TACGCCCGCC CAATAAGGCT ACTGGCGGG CCGTCGAAGG CCGTTTGTT 2110
2111 TCAGAAACCC AAGCCCCCCC TCATACCAAC GTTTCGACTT TGATTCTTGC CGGTACGTGG TGGTGGGTGC 2180
2181 CTTAGCTCTT TCTCGATAGT TAG AC

Fig. 3a

28S -
L3G25#4 →
18S -

K46
EL4 TPA
L3
L3 ConA
LGL

Fig. 3b

28S -
L3G14#2 →
18S -

K46
EL4 TPA
L3
L3 ConA
LGL

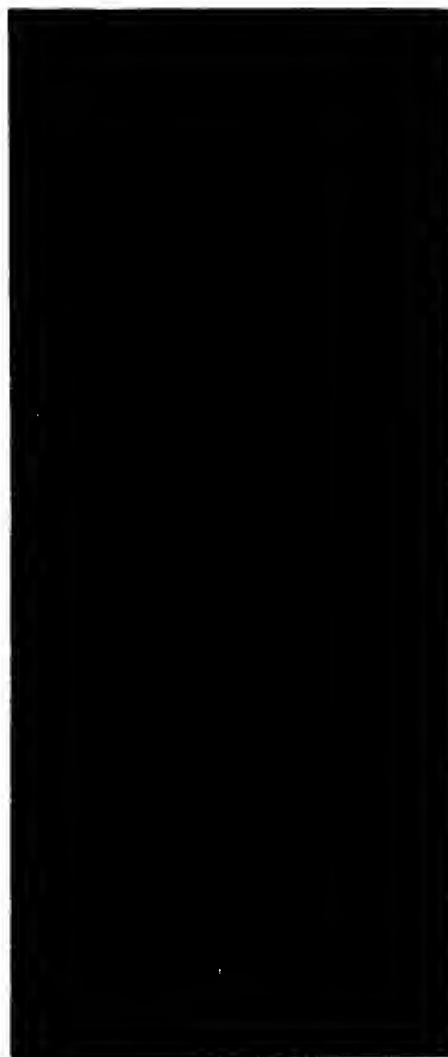
Fig. 3c

L3G20#3

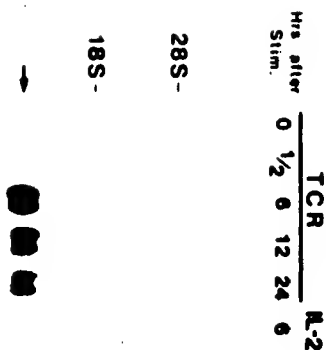
28S -
18S -

K46
EL4 TPA
L3
L3 ConA
LGL

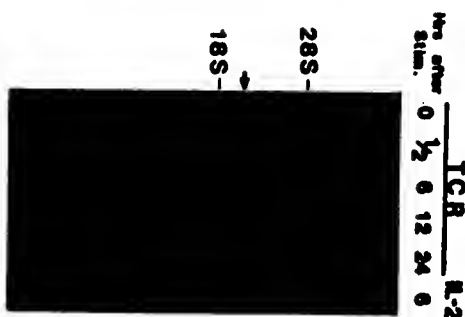
Fig. 4

1 2 3 4**-21.7****-5.2****-2.0**

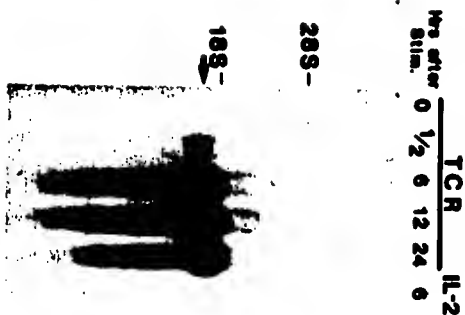
a Fig. 6a



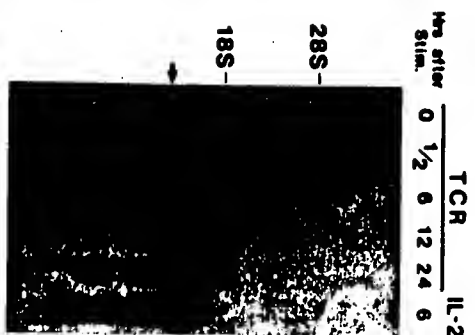
b Fig. 6b

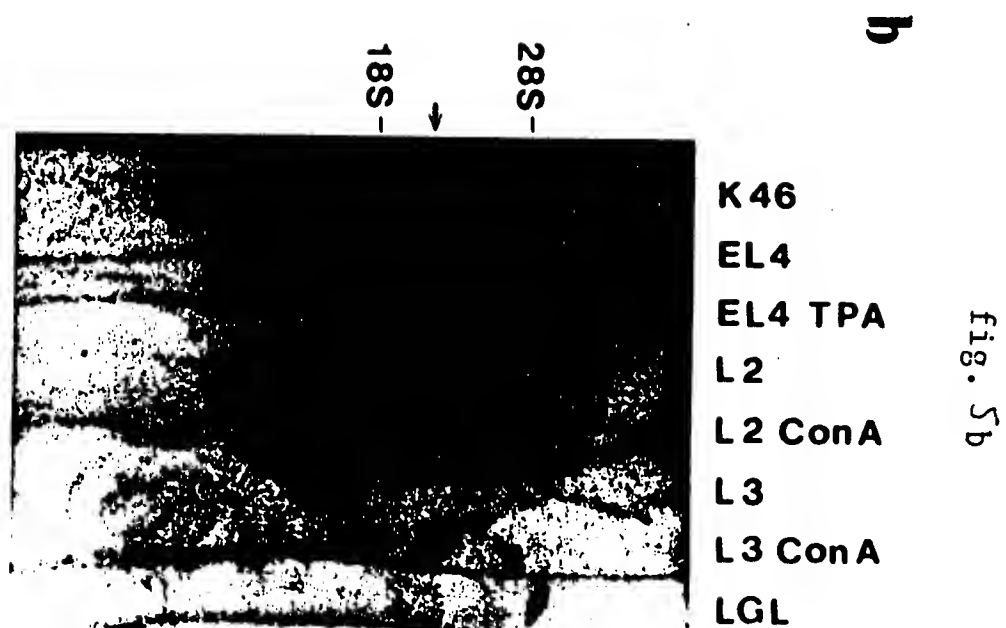
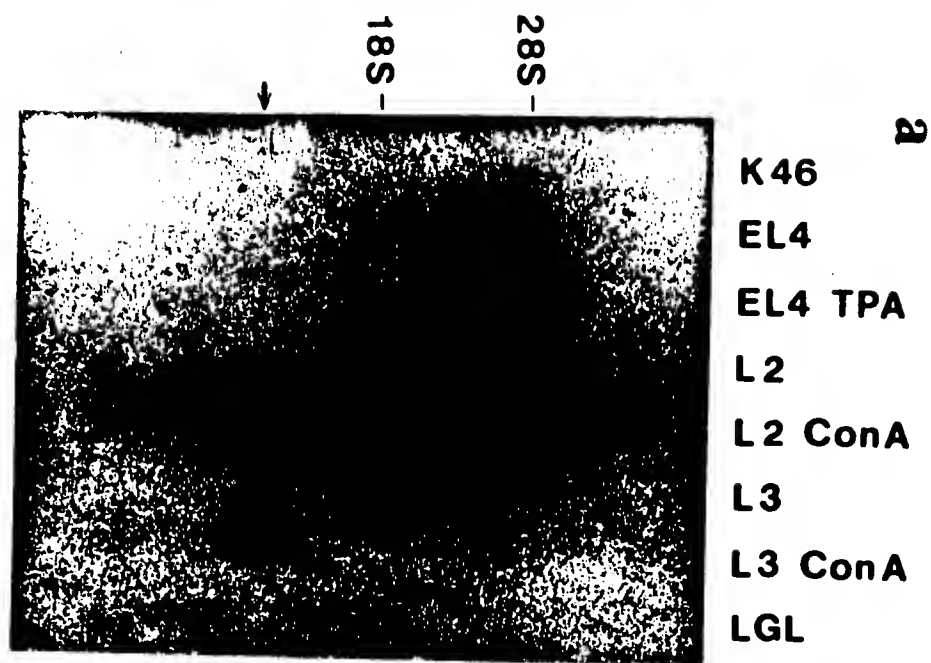


c Fig. 6c



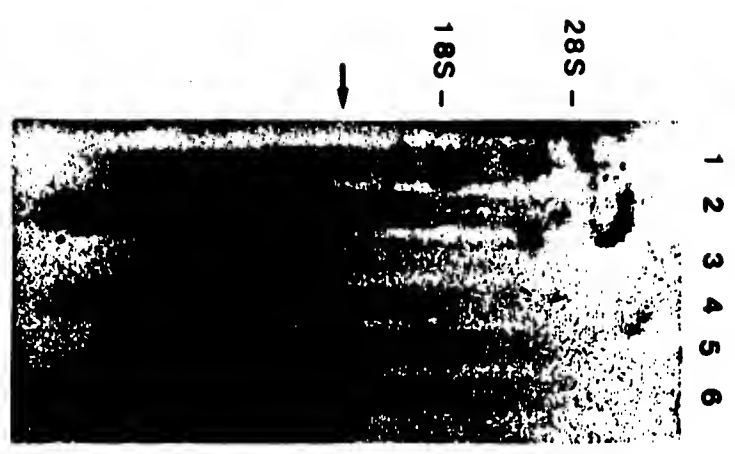
d Fig. 6d





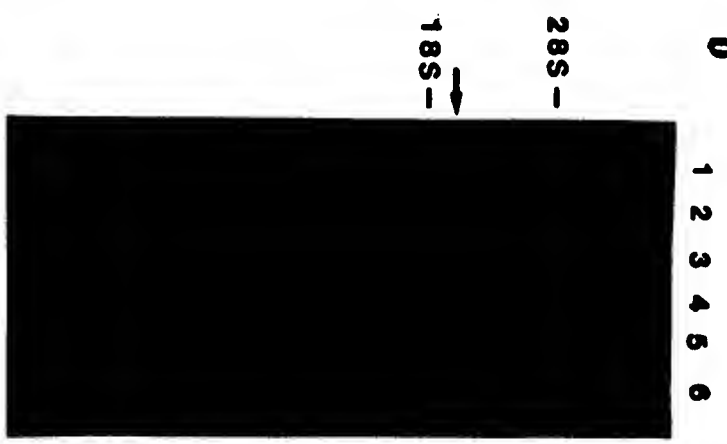
a

Fig. 7a



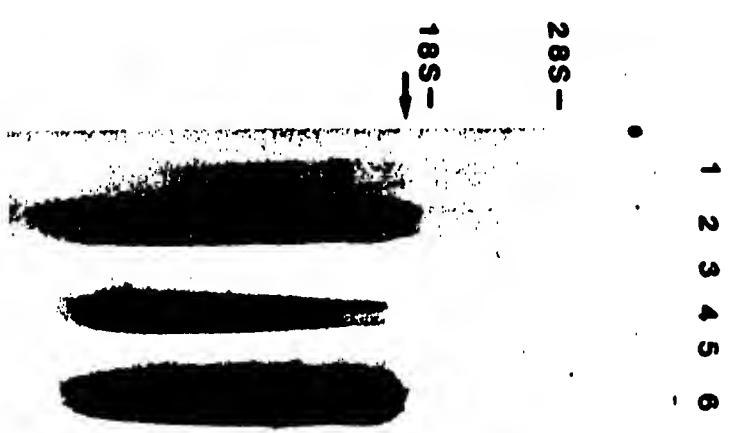
b

Fig. 7b



c

Fig. 7c



a



Fig. 8a

b

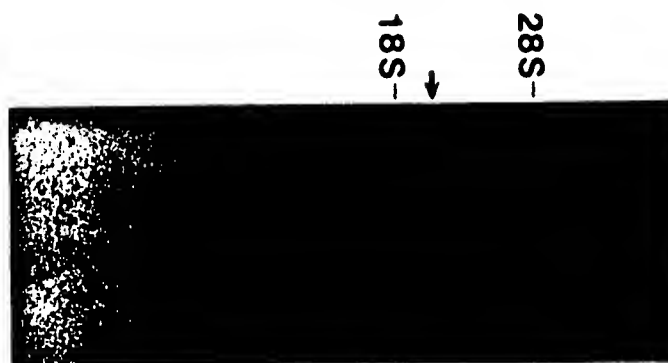


Fig. 8b

BW5147
BW5147 ConA
Md90
Md90 ConA
PN37
PN37 ConA

L2
A11
L3
Melanocyte

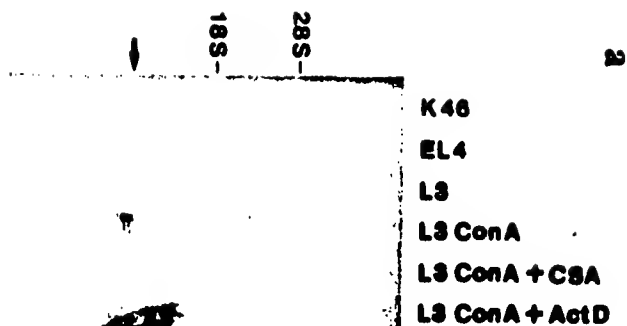


Fig. 9a

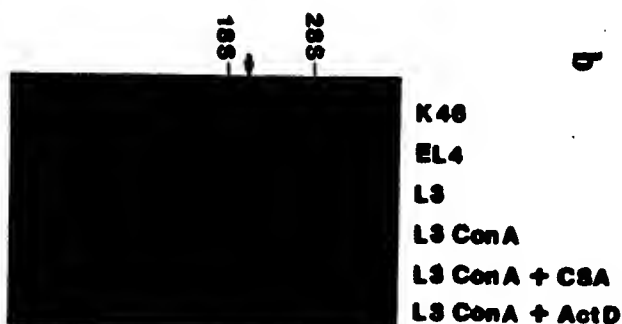


Fig. 9b

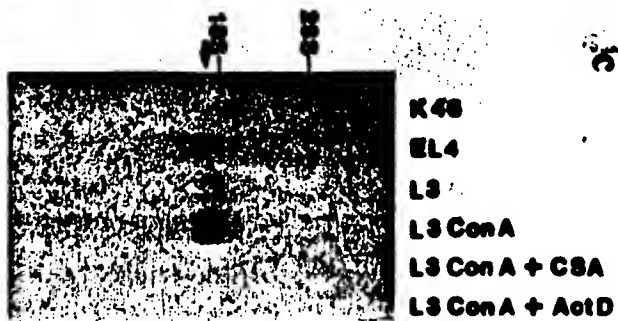


Fig. 9c

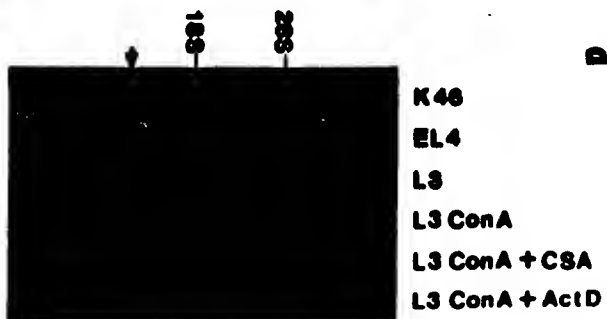


Fig. 9d

DR 112269

a

Fig. 10a

1 2 3 4

28S -

18S -



b

Fig. 10b

1 2 3 4

28S -

18S -



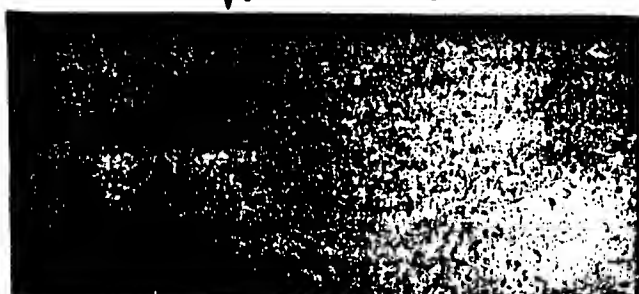
c

Fig. 10c

1 2 3 4

28S -

18S -



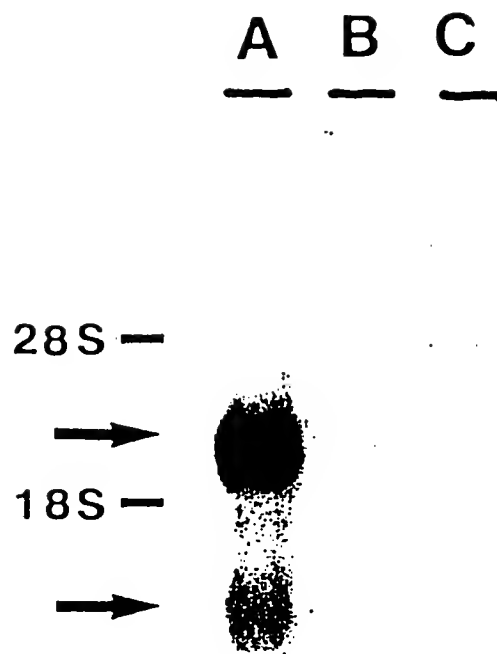


Figure 11

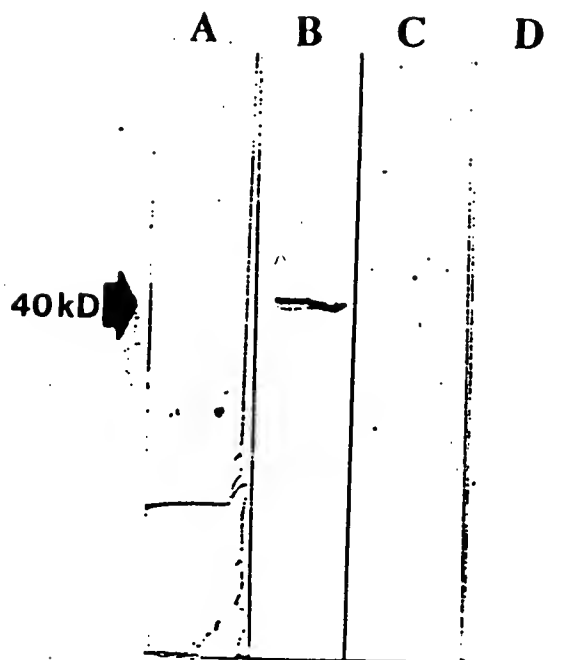


Figure 12

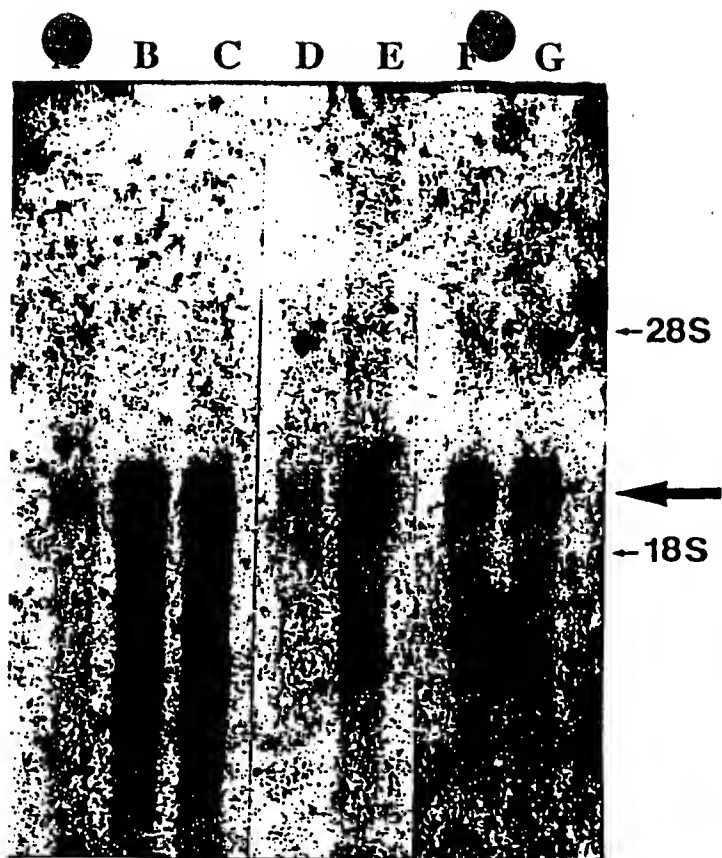


Figure 15

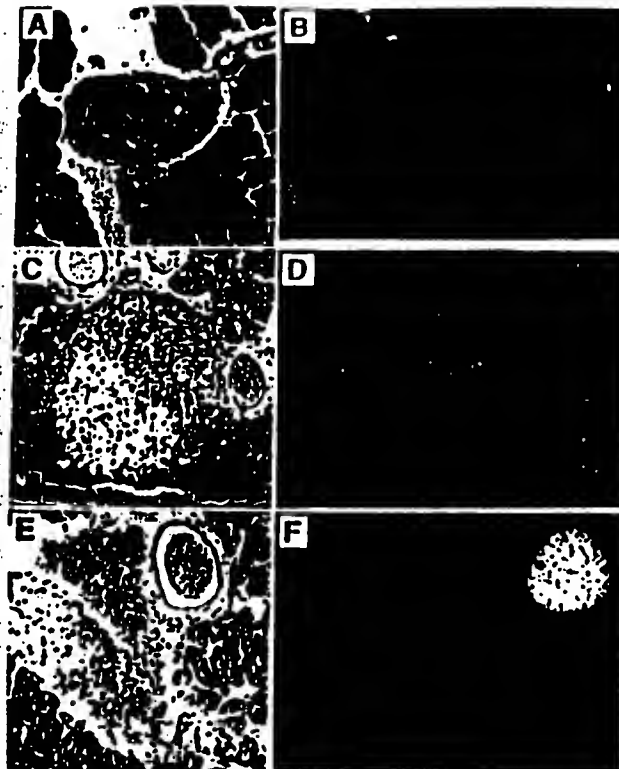


Figure 16

Figure 17

4-1BB	(64)	C	R	V	C	A	G	Y	F	R	F	K	K	-	-	F	-	C	S	S	T	H	N	A	E	C	-	E	C
Sina	(71)	C	P	V	C	F	D	Y	V	-	-	-	-	I	L	Q	C	S	S	G	H	L	V	-	C	V	S	C	
DG17	(25)	C	P	I	C	F	E	F	I	-	Y	K	K	Q	I	Y	Q	C	K	S	G	H	H	A	-	C	K	E	C

Fig. 18

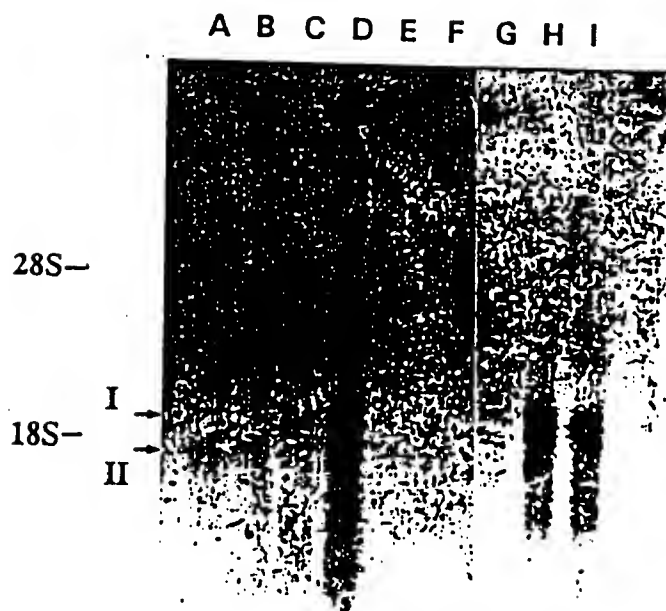


Fig 19.

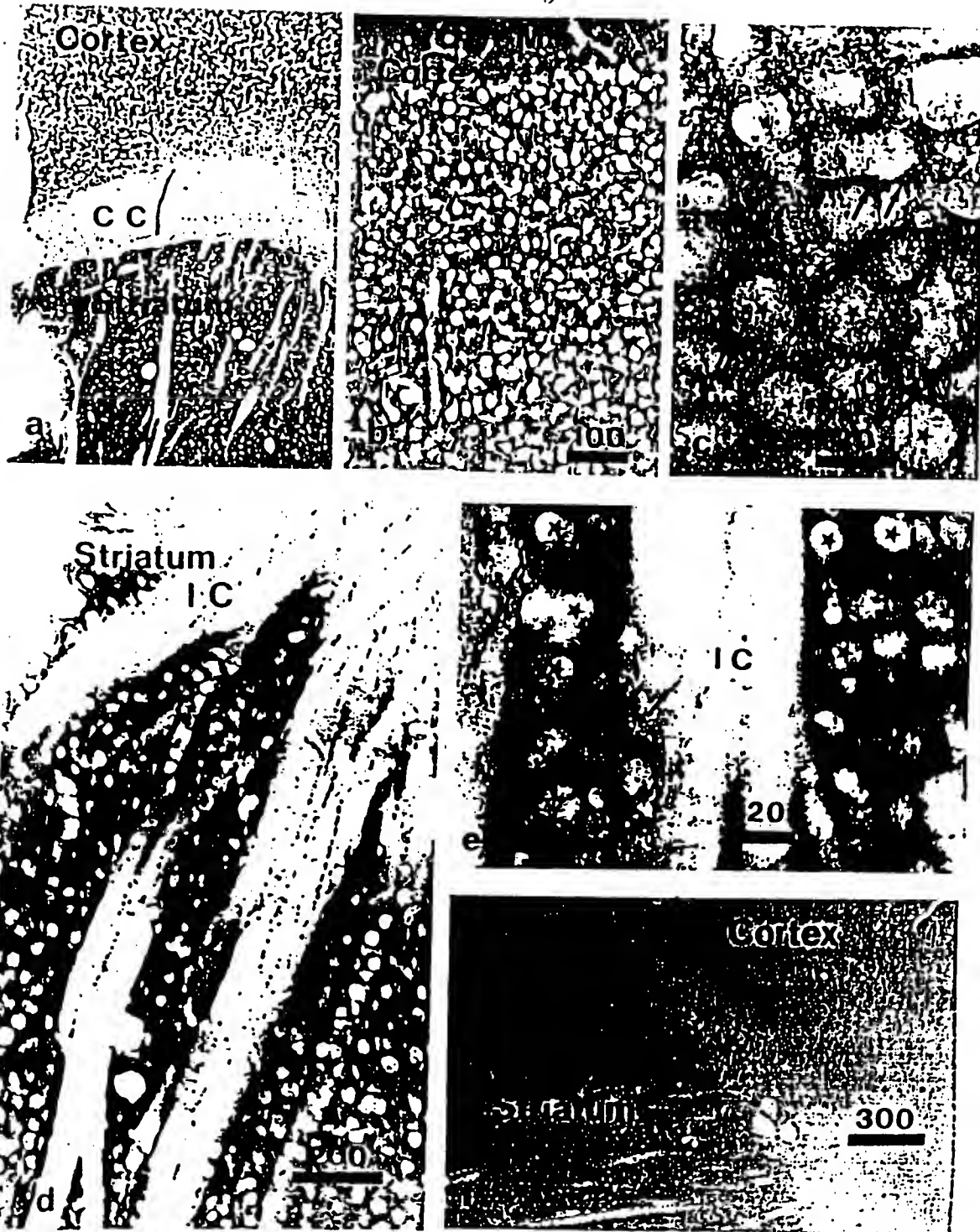
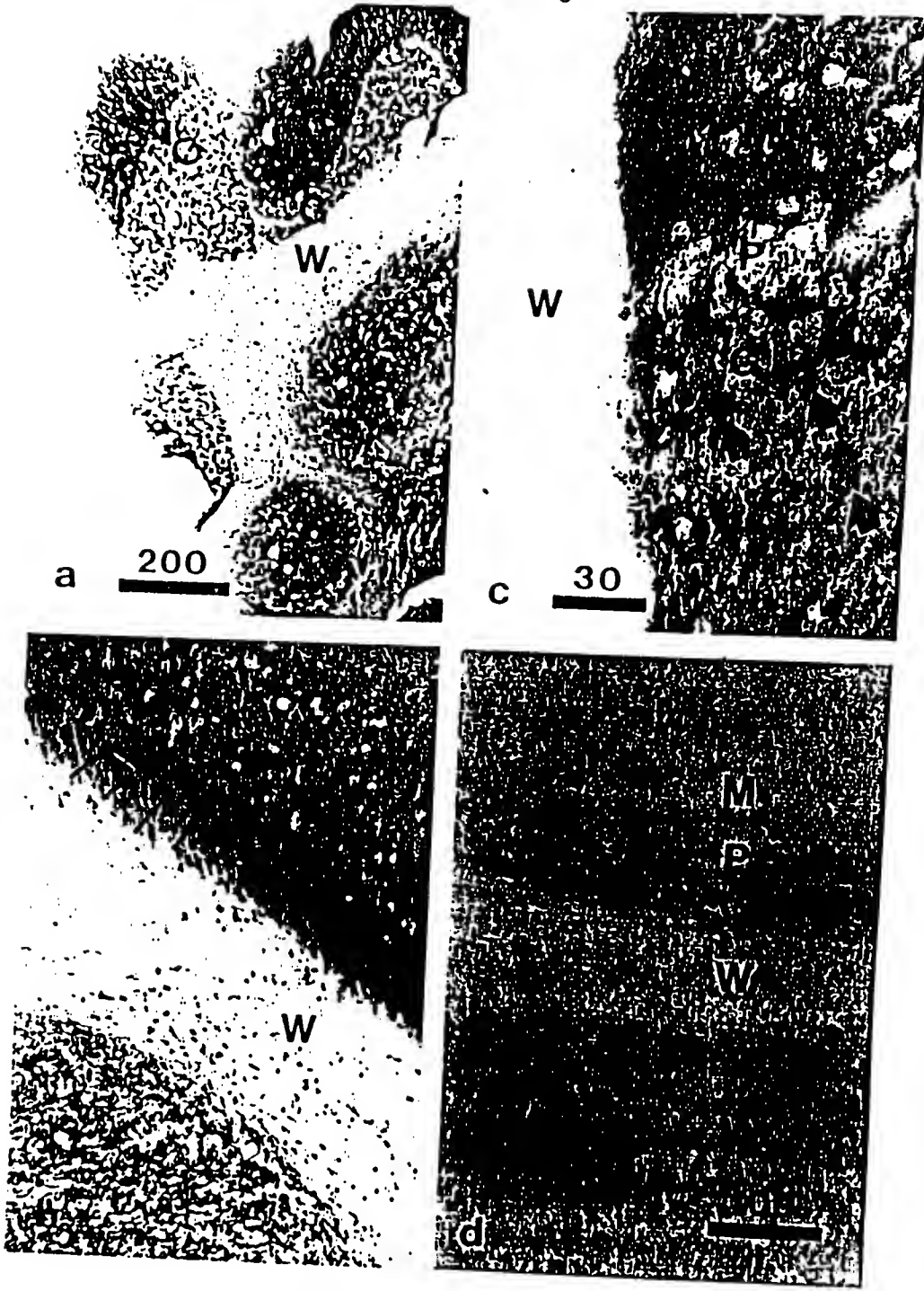


Fig. 20



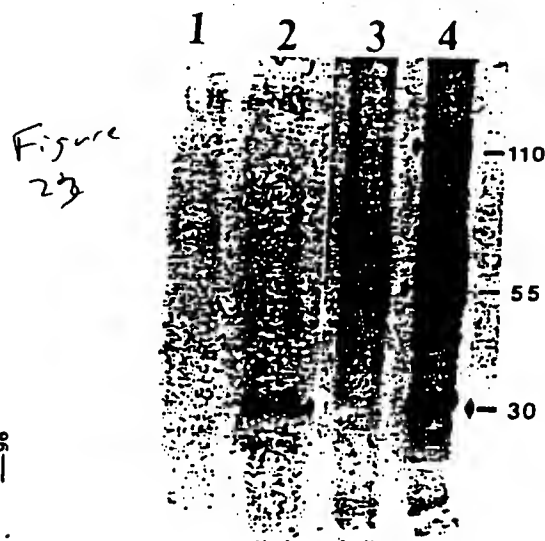
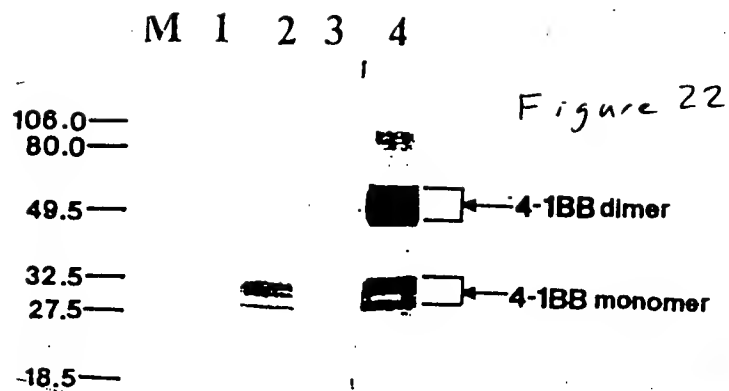
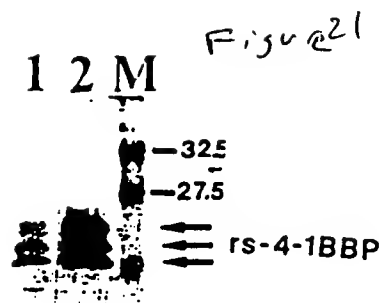


Figure 25

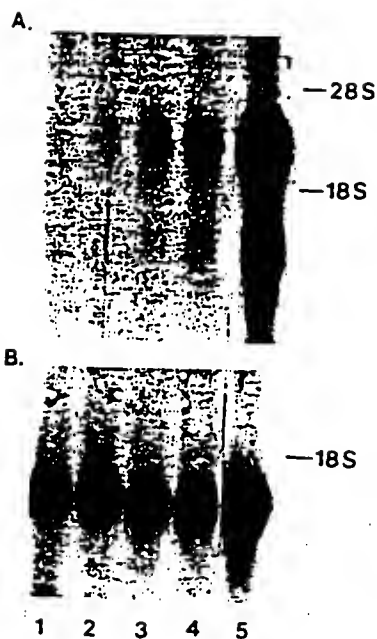


Figure 26



Figure 27

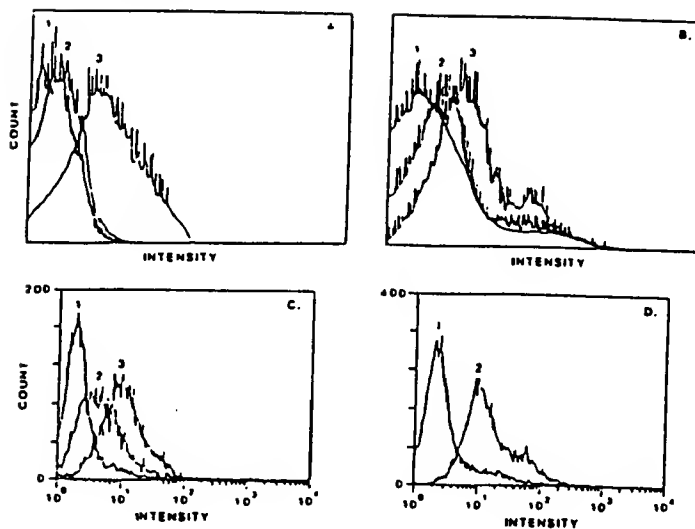


Figure 28

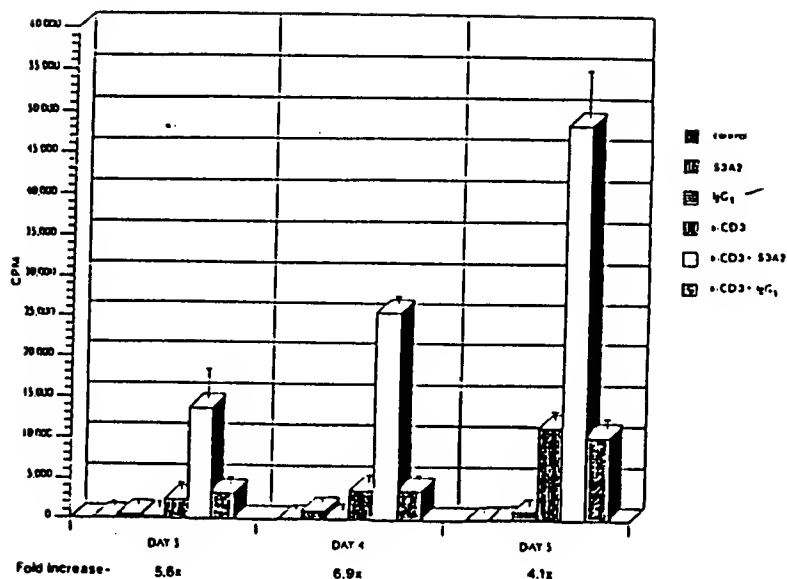


Figure 29

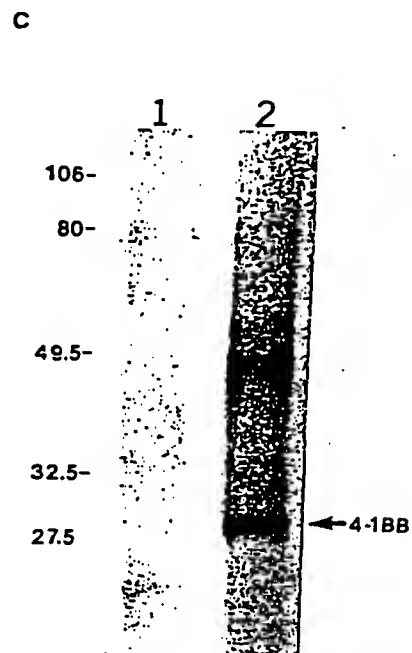
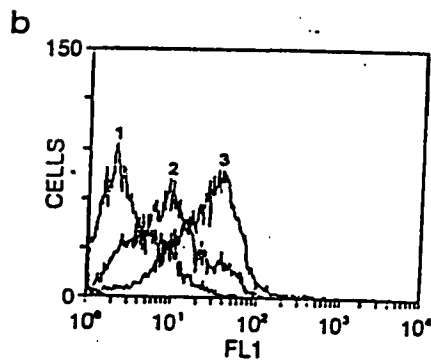
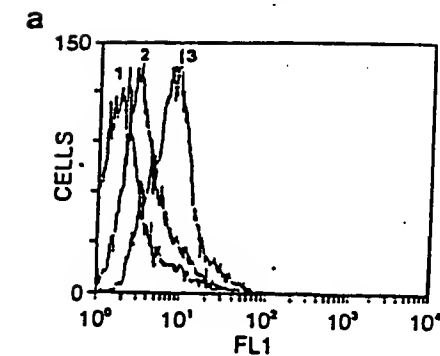


Figure 30

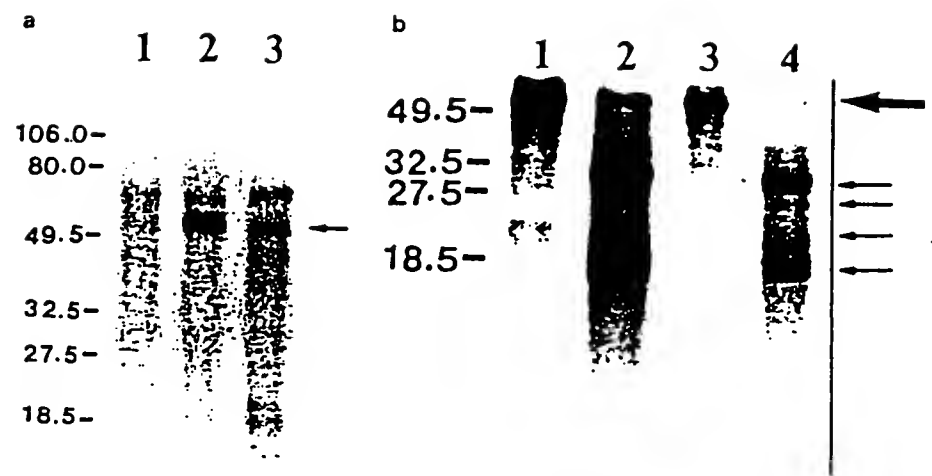
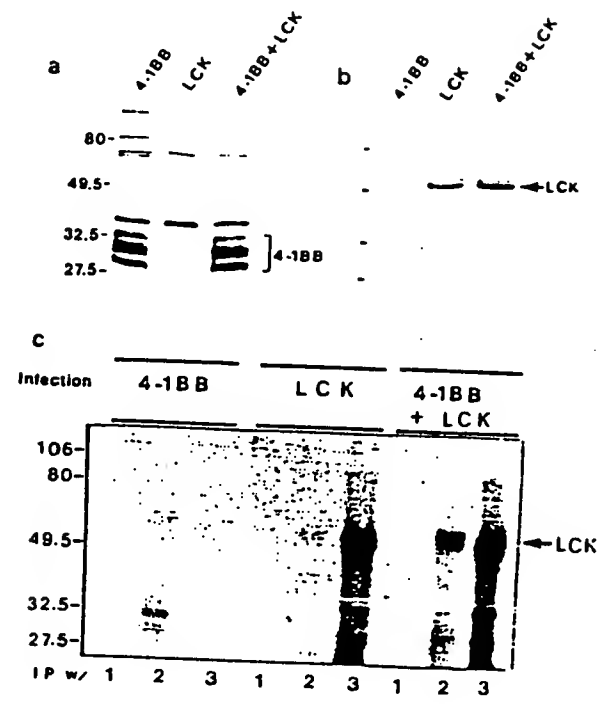


Figure 31



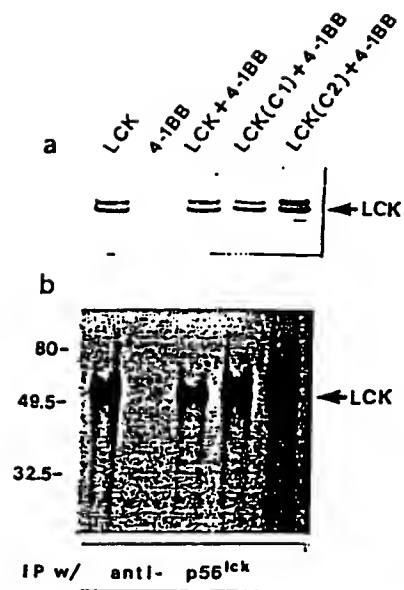


Figure 32

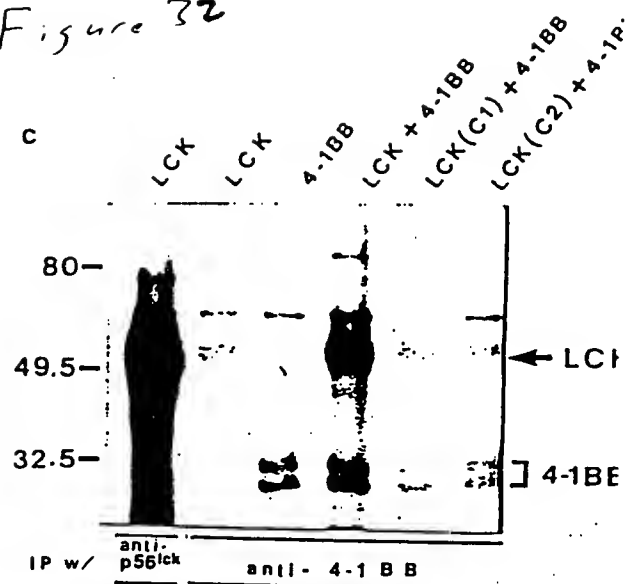


Figure 33

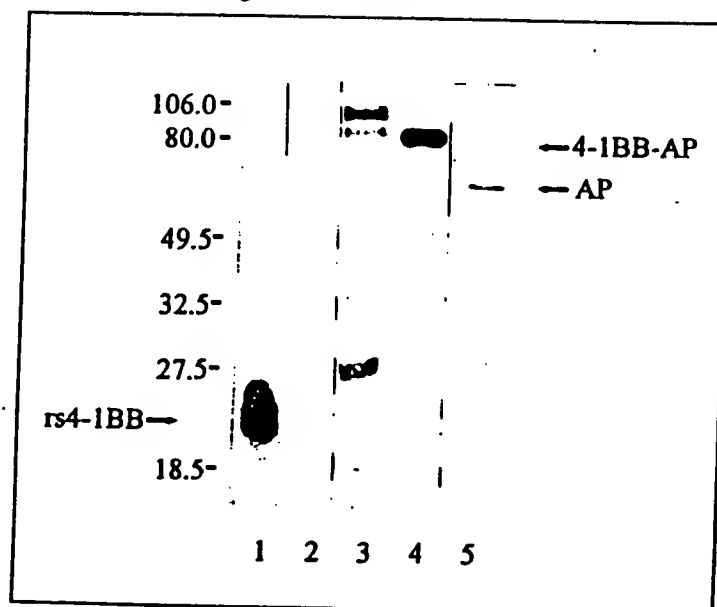


Figure 3Ha

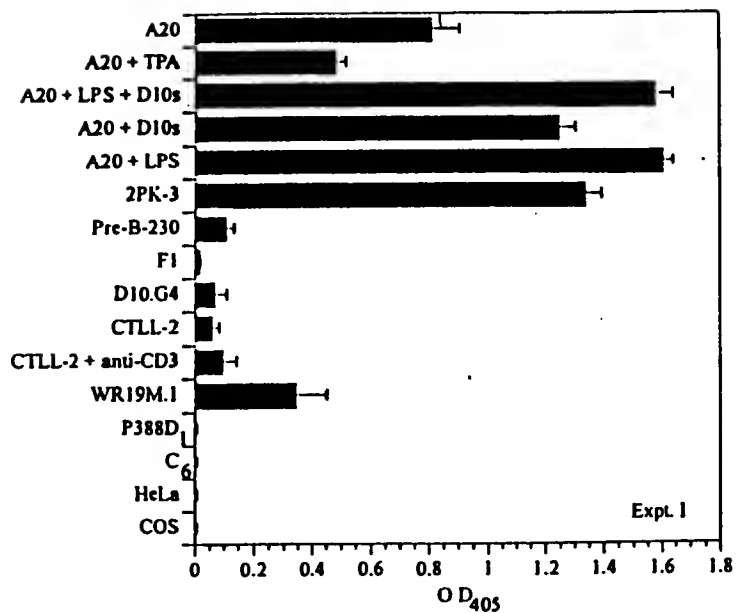


Figure 3Hb

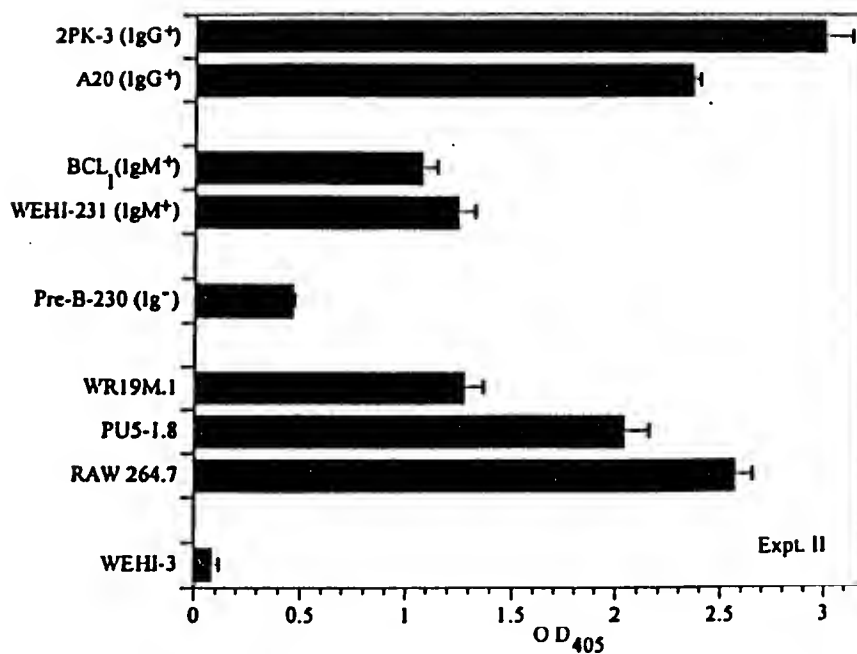


Figure 37c

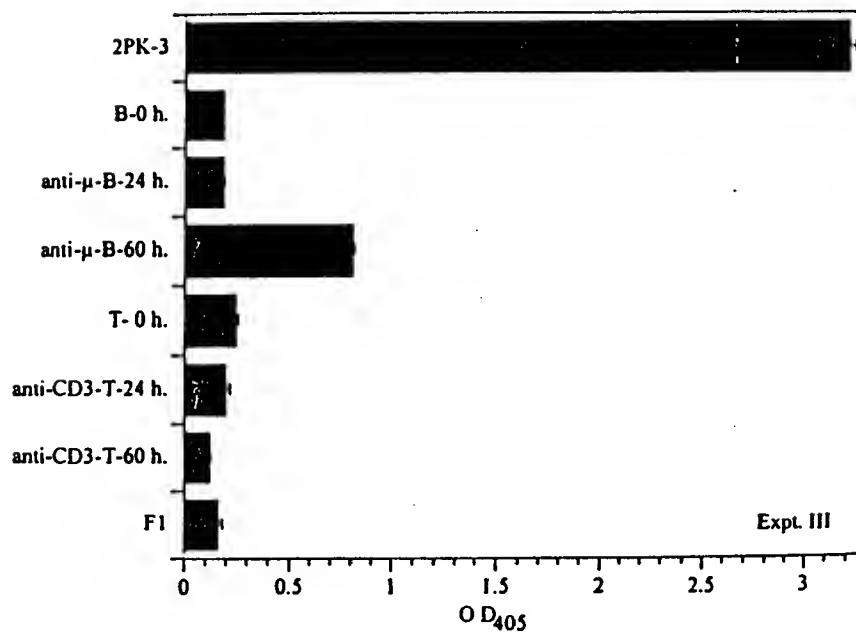


Figure 35a

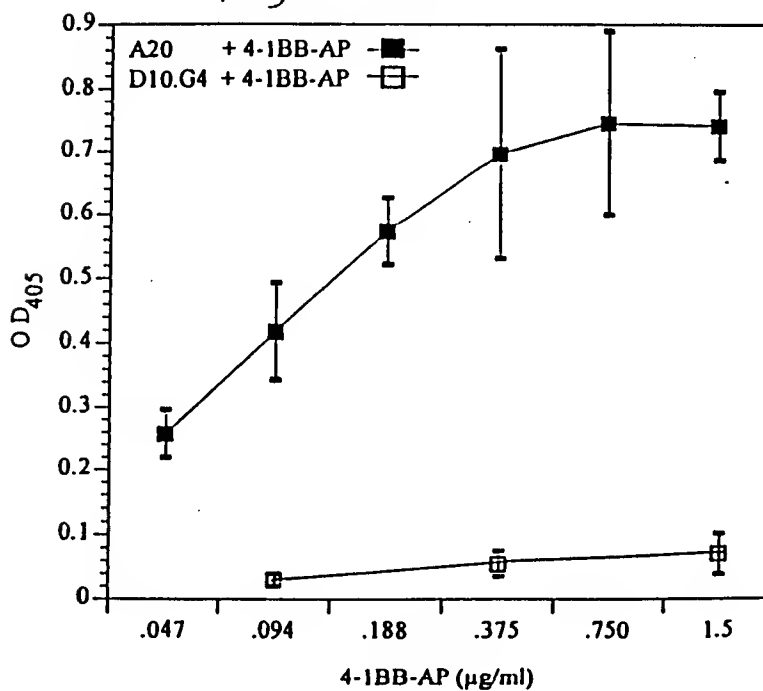


Figure 35b

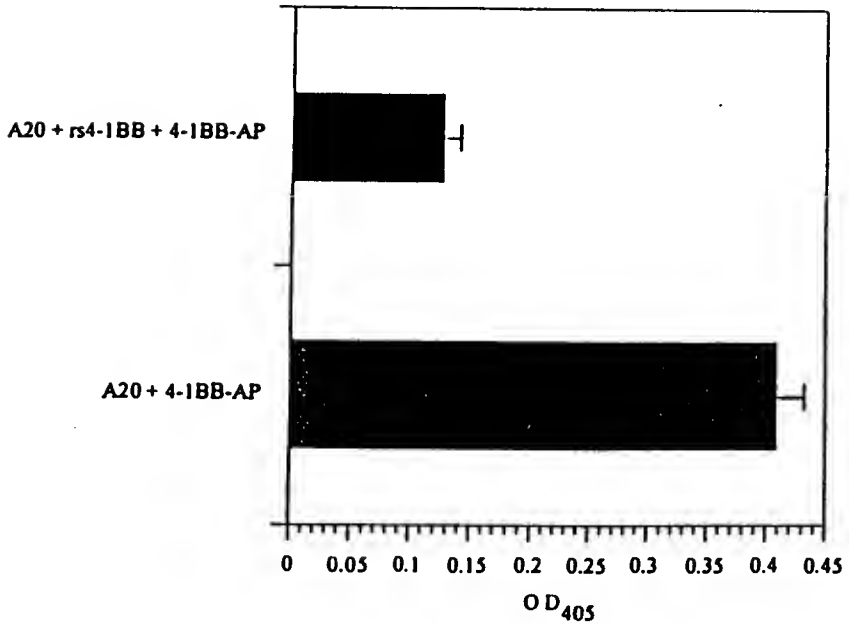


Figure 36

